NCBI   results of **BLAST**

INFO: Entrez query "AF152376" returned no records, with error: NULL returned from EntrezSynchronousQuery()
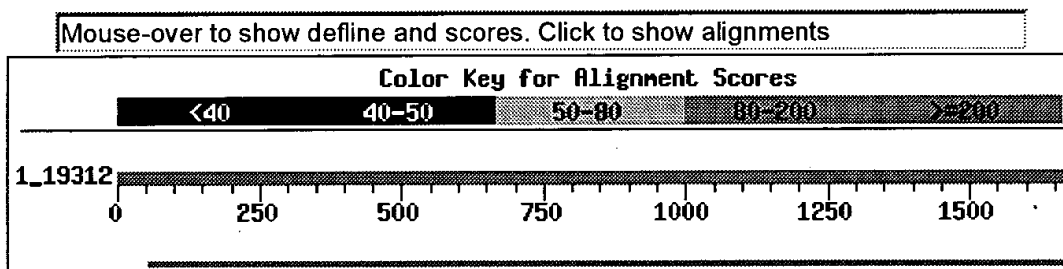

BLASTN 2.2.6 [Apr-09-2003]

RID: 1061432177-19312-234002.BLASTQ3

Query= gi|5870623|gb|AF084467.1|AF084467
          (1669 letters)

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, or phase 0, 1 or 2 HTGS sequences)
          1,879,486 sequences; 8,891,580,893 total letters

Taxonomy reports

Distribution of 2 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments

Color Key for Alignment Scores				
<40	40-50	50-80	80-200	>=200

1_19312

0   250   500   750   1000   1250   1500

| | Score | E |
Sequences producing significant alignments:	(bits)	Value
gi|5616196|gb|AF152376.1|AF152376 Homo sapiens heparanase m...	3126	0.0

Alignments

| Get selected sequences | Select all | Deselect all |

☐ >gi|5616196|gb|AF152376.1|AF152376   Homo sapiens heparanase mRNA, complete cds
          Length = 1694

Score = 3126 bits (1577), Expect = 0.0
Identities = 1605/1616 (99%), Gaps = 3/1616 (0%)
Strand = Plus / Plus

Query: 54   cctggggccgctgggtccctctcccctggcgccctgccccgacctgcgcaagcacagca 113
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

```
Sbjct: 65    cctggggccgctgggtccctctccctggcgccctgccccgacctgcgcaagcacag-- 122

Query: 114   ggacgtcgtggacctggacttcttcacccaggagccgctgcacctggtgagcccctcgtt 173
             ||||||||||||||||||||||||||||||||.|||||||||||||||||||||||||||
Sbjct: 123   -gacgtcgtggacctggacttcttcacccaggagccgctgcacctggtgagcccctcgtt 181

Query: 174   cctgtccgtcaccattgacgccaacctggccacggacccgcggttcctcatcctcctggg 233
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 182   cctgtccgtcaccattgacgccaacctggccacggacccgcggttcctcatcctcctggg 241

Query: 234   ttctccaaagcttcgtaccttggccagaggcttgtctcctgcgtacctgaggtttggtgg 293
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 242   ttctccaaagcttcgtaccttggccagaggcttgtctcctgcgtacctgaggtttggtgg 301

Query: 294   caccaagacagacttcctaattttcgatcccaagaaggaatcaacctttgaagagagaag 353
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 302   caccaagacagacttcctaattttcgatcccaagaaggaatcaacctttgaagagagaag 361

Query: 354   ttactggcaatctcaagtcaaccaggatatttgcaaatatggatccatccctcctgatgt 413
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 362   ttactggcaatctcaagtcaaccaggatatttgcaaatatggatccatccctcctgatgt 421

Query: 414   ggaggagaagttacggttggaatggccctaccaggagcaattgctactccgagaacacta 473
             |||||||||||.||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 422   ggaggagaagttacggttggaatggccctaccaggagcaattgctactccgagaacacta 481

Query: 474   ccagaaaaagttcaagaacagcacctactcaagaagctctgtagatgtgctatacacttt 533
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 482   ccagaaaaagttcaagaacagcacctactcaagaagctctgtagatgtgctatacacttt 541

Query: 534   tgcaaactgctcaggactggacttgatctttggcctaaatgcgttattaagaacagcaga 593
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 542   tgcaaactgctcaggactggacttgatctttggcctaaatgcgttattaagaacagcaga 601

Query: 594   tttgcagtggaacagttctaatgctcagttgctcctggactactgctcttccaaggggta 653
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 602   tttgcagtggaacagttctaatgctcagttgctcctggactactgctcttccaaggggta 661

Query: 654   taacatttcttgggaactaggcaatgaacctaacagtttccttaagaaggctgatatttt 713
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 662   taacatttcttgggaactaggcaatgaacctaacagtttccttaagaaggctgatatttt 721

Query: 714   catcaatgggtcgcagttaggagaagatttttattcaattgcataaacttctaagaaagtc 773
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 722   catcaatgggtcgcagttaggagaagatttttattcaattgcataaacttctaagaaagtc 781

Query: 774   caccttcaaaaatgcaaaactctatggtcctgatgttggtcagcctcgaagaaagacggc 833
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 782   caccttcaaaaatgcaaaactctatggtcctgatgttggtcagcctcgaagaaagacggc 841
```

```
Query: 834   taagatgctgaagagcttcctgaaggctggtggagaagtgattgattcagttacatggca 893
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 842   taagatgctgaagagcttcctgaaggctggtggagaagtgattgattcagttacatggca 901


Query: 894   tcactactatttgaatggacggactgctaccagggaagatttttctaaaccctgatgtatt 953
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 902   tcactactatttgaatggacggactgctaccagggaagatttttctaaaccctgatgtatt 961


Query: 954   ggacatttttatttcatctgtgcaaaaagttttccaggtggttgagagcaccaggcctgg 1013
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 962   ggacatttttatttcatctgtgcaaaaagttttccaggtggttgagagcaccaggcctgg 1021


Query: 1014  caagaaggtctggttaggagaaacaagctctgcatatggaggcggagcgcccttgctatc 1073
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1022  caagaaggtctggttaggagaaacaagctctgcatatggaggcggagcgcccttgctatc 1081


Query: 1074  cgacacctttgcagctggctttatgtggctggataaaattgggcctgtcagcccgaatggg 1133
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1082  cgacacctttgcagctggctttatgtggctggataaaattgggcctgtcagcccgaatggg 1141


Query: 1134  aatagaagtggtgatgaggcaagtattctttggagcaggaaactaccatttagtggatga 1193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1142  aatagaagtggtgatgaggcaagtattctttggagcaggaaactaccatttagtggatga 1201


Query: 1194  aaacttcgatcctttacctgattattggctatctcttctgttcaagaaattggtgggcac 1253
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1202  aaacttcgatcctttacctgattattggctatctcttctgttcaagaaattggtgggcac 1261


Query: 1254  caaggtgttaatggcaagcgtgcaaggttcaaagagaaggaagcttcgagtataccttca 1313
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1262  caaggtgttaatggcaagcgtgcaaggttcaaagagaaggaagcttcgagtataccttca 1321


Query: 1314  ttgcacaaacactgacaatccaaggtataaagaaggagatttaactctgtatgccataaa 1373
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1322  ttgcacaaacactgacaatccaaggtataaagaaggagatttaactctgtatgccataaa 1381


Query: 1374  cctccataacgtcaccaagtacttgcggttaccctatcctttttctaacaagcaagtgga 1433
              |||||||||  |||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1382  cctccataatgtcaccaagtacttgcggttaccctatcctttttctaacaagcaagtgga 1441


Query: 1434  taaataccttctaagacctttgggacctcatggattactttccaaatctgtccaactcaa 1493
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1442  taaataccttctaagacctttgggacctcatggattactttccaaatctgtccaactcaa 1501


Query: 1494  tggtctaactctaaagatggtggatgatcaaaccttgccacctttaatggaaaaacctct 1553
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1502  tggtctaactctaaagatggtggatgatcaaaccttgccacctttaatggaaaaacctct 1561


Query: 1554  ccggccaggaagttcactgggcttgccagctttctcatatagnnnnnnngtgataagaaa 1613
              |||||||||||||||||||||||||||||||||||||||||||         |||||||||||
Sbjct: 1562  ccggccaggaagttcactgggcttgccagctttctcatatagtttttttgtgataagaaa 1621
```

```
Query: 1614 tgccaaagttgctgcttgcatctgaaaataaaatatactagtcctgacactgaaaa 1669
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1622 tgccaaagttgctgcttgcatctgaaaataaaatatactagtcctgacactgaaaa 1677
```

```
 Score = 28.2 bits (14), Expect = 0.009
 Identities = 14/14 (100%)
 Strand = Plus / Minus
```

```
Query: 380 atatttgcaaatat 393
            ||||||||||||||
Sbjct: 401 atatttgcaaatat 388
```

| Get selected sequences | Select all | Deselect all |

```
  Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS,
  or phase 0, 1 or 2 HTGS sequences)
     Posted date:  Aug 20, 2003 12:00 AM
  Number of letters in database: -24,009,540
  Number of sequences in database:  1,779,461
```

```
Lambda      K       H
    1.37     0.711     1.31
```

```
Gapped
Lambda      K       H
    1.37     0.711     1.31
```

```
Matrix: blastn matrix:1 -3
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 0
Number of Sequences: 100025
Number of extensions: 0
Number of successful extensions: 0
Number of sequences better than 10.0: 0
Number of HSP's better than 10.0 without gapping: 0
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 0
length of query: 3340
length of database: 1694
effective HSP length: 10
effective length of query: 1659
effective length of database: 1684
effective search space:  2793756
effective search space used:  2793756
T: 0
A: 0
X1: 6 (11.9 bits)
X2: 15 (29.7 bits)
S1: 12 (24.3 bits)
S2: 9 (18.3 bits)
```